

GenCore version 5.1.6
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score greater than or equal to the score of the result being printed.
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	135.8	27.1	AP05958	Bradyrhizobium sp.
C 2	97.2	19.4	AB011858	Xanthomonas campestris subsp. campestris
C 3	92.4	18.4	AF273216	Rhizobium sp.
C 4	88.8	17.7	SDS51197	Sphingomonas sp.
C 5	88.8	17.7	AR068625	Sequence
C 6	87.6	17.5	AB012538	Xylella fastidiosa
C 7	86.8	17.3	AB012558	Xylella fastidiosa
C 8	86	17.2	NMB391263	Neisseria gonorrhoeae
C 9	86	17.2	AF121772	Neisseria gonorrhoeae
C 10	86	17.2	NMB391260	Neisseria gonorrhoeae
C 11	86	17.2	AB002524	Neisseria gonorrhoeae
C 12	86	17.2	AL62257	Neisseria gonorrhoeae
C 13	86	17.2	NM4622491	Neisseria gonorrhoeae
C 14	86	17.2	AX044033	Sequence
C 15	80.6	16.1	AB016792	Pseudomonas aeruginosa
C 16	80.4	16.0	AL646077	Ralstonia eutropha
C 17	69.8	13.9	AB013811	Yersinia enterocolitica
C 18	69.8	13.9	AJ41451	Yersinia enterocolitica
C 19	67.4	13.5	AP005959	Bradyrhizobium sp.
C 20	62.6	12.5	BPCYADE	Bradyrhizobium sp.
C 21	56.8	11.3	AF193064	Caulobacter
C 22	56.8	11.3	AB005779	Caulobacter
C 23	56.8	11.3	AF62345	Caulobacter
C 24	54.2	10.8	AL939118	Serratomyces cerevisiae
C 25	53.2	10.6	AL646083	Ralstonia eutropha
C 26	52.6	10.5	AY158231	Caulobacter
C 27	52	10.4	AK55393	Sequence
C 28	51.6	10.3	AE062345	A. pleurospira
C 29	51.6	10.3	X68595	A. pleurospira
C 30	51.6	10.3	AR091872	Sequence
C 31	51.6	10.3	AR268551	Sequence
C 32	51.2	10.2	AP05038	Streptomyces
C 33	48.6	9.7	AP03007	Mesorhizobium
C 34	48.4	9.7	M65808	Actinobacillus
C 35	48	9.6	X64558	P. aeruginosa
C 36	48	9.6	AE004554	Pseudomonas
C 37	47.8	9.5	E30060	ABC transporter
C 38	47.8	9.5	AB023289	Pseudomonas
C 39	47.6	9.5	AE004761	Pseudomonas
C 40	47.2	9.4	AL591786	Sinorhizobium
C 41	47	9.4	AB006947	Mycobacterium
C 42	47	9.4	284724	Mycobacterium
C 43	47	9.4	MTCTY22G10	Mycobacterium
C 44	47	9.4	MSGV423	Mycobacterium
C 45	46.8	9.3	BX248335	Mycobacterium
C 46	46.8	9.3	AF416330	Ruegeria

ALIGNMENTS

RESULT	1			
LOCUS	AP05958/c	302650 bp	DNA	BCT 28-MAR-2003
DEFINITION	Bradyrhizobium japonicum USDA 110 DNA, complete genome, section 24/31.			
ACCESSION	AP05958	BA00040		
VERSION	AP05958.1	GT:27354550		
KEYWORDS				
SOURCE				
ORGANISM	Bradyrhizobium japonicum USDA 110			
	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
	Bradyrhizobiaceae; Bradyrhizobium.			
REFERENCE	Kaneo,T., Nakamura,Y., Sato,S., Minamisawa,K., Uchiumi,T., Kawashima,K., Sasamoto,S., Watanabe,A., Idesawa,K., Iriuchi,M.,			
AUTHORS				

Pred. No. is the number of results predicted by chance to have a

Kohara, M., Matsumoto, M., Shimpo, S., Tsuruoka, H., Wada, T., Yamada, M., and Tabata, S.		gene
Complete Genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA10	CDS	
JOURNAL DNA Res. 9 (6), 189-197 (2002)		
MEDLINE 22446998		
PUBLMED 12591275		
REFERENCE 2		
AUTHORS Kaneko, T., Nakamura, Y., Saro, S., Minamisawa, K., Uchiumi, T., Sasamoto, S., Watanabe, A., Idesawa, K., Iriuchi, M., Kawashima, K., Kohara, M., Matsumoto, M., Shimpo, S., Tsuruoka, H., Wada, T., Yamada, M., and Tabata, S.		
TITLE Complete Genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA10 (supplement)		
JOURNAL DNA Res. 9 (6), 225-256 (2002)		
MEDLINE 2245002		
PUBLMED 12591279		
REFERENCE 3 (bases 1 to 302650)		
AUTHORS Kaneko, T.		gene
TITLE Direct Submission		
JOURNAL Submitted (20-NOV-2002) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; 2-6-7 Kazusa-kamatachi, Kasarazu, Chiba 292-0812, Japan		
(E-mail: kanekokazusa.or.jp,		
URL: http://www.kazusa.or.jp/rhizobase/, Tel: +81-438-52-3935, Fax: +81-438-52-3934)		
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/mol type="Genomic DNA"		
/stran="USDA110"		
/db_xref="taxon:224911"		
gene 31..1110		
/gene="blr6272"		
/note="AraC family		
ORF ID:blr6272"		
/codon_start=1		
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/protein_id="BAC51537.1"		
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gene 7084..7085		
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/note="ORF ID:blr6278"		
/codon_start=1		
/transl_table=11		

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	(without alignments)
	7352.985 Million cell updates/sec
Title:	US-09-484-577a-3
Perfect score:	501
Sequence:	1 actctccaggcttcaccga.....cagaatgcggcgatgtatcat 501
Scoring table:	IDENTITY_NUC
	Gapp 10.0 , Gapext 1.0
Searched:	22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters:	455562784
Minimum DB seq length:	0
Maximum DB seq length:	20000000000
Post-processing:	Minimum Match 0\$
	Maximum Match 100\$
	Listing first 45 summaries
Database :	EST:*
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	2: em_estbum:*
	3: em_estin:*
	4: em_estmu:*
	5: em_estov:*
	6: em_estpl:*
	7: em_estro:*
	8: em_ntcc:*
	9: gb_est1:*
	10: gb_est2:*
	11: gb_ntcc:*
	12: gb_est3:*
	13: gb_est4:*
	14: gb_est5:*
	15: em_estfun:*
	16: em_estom:*
	17: em_gss_hum:*
	18: em_gss_inv:*
	19: em_gss_pln:*
	20: em_gss_vrt:*
	21: em_gss_fun:*
	22: em_gss_mam:*
	23: em_gss_mus:*
	24: em_gss_pro:*
	25: em_gss_fod:*
	26: em_gss_phg:*
	27: em_gss_vri:*
	28: gb_gss1:*
	29: gb_gss2:*

ALIGNMENTS

RESULT	CNS0070E/c	DNA	linear	GSS 03-JUN-1999
LOCUS	Drosophila melanogaster genome survey sequence TET3	932 bp		end of BAC #
DEFINITION	BACR14D21 of RPCI-98 library from Drosophila melanogaster (fruit fly)			BACR14D21 of RPCI-98 library from Drosophila melanogaster (fruit fly)
ACCESSION	AL066254			Genomic survey sequence.
VERSION	GI:4945121			
KEYWORDS	GSS.			
SOURCE	Drosophila melanogaster			
ORGANISM	Drosophila melanogaster			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyditoidea; Drosophilidae; Drosophila.			
AUTHORS	1 (bases 1 to 932)			
TITLE	Genoscope - Centre National de Séquençage : Direct Submission			
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage : BP 191 91006 ERY cedex PRANCE (E-mail : seqref@genoscope.cnrs.fr)			
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org . The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammone in Pieter de Jong's laboratory in the Department of			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
c 1	60.6	12.1	932	CNS0070E
c 2	55	11.0	925	CNS0070E
c 3	49.4	9.9	812	B2549462
c 4	45.2	9.0	1148	BX374895

FEATURES	Source	BASE COUNT	ORIGIN	Query Match	Score	DB	Length	Qualifiers
		6	bw	1. .925 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACR1916" /clone_id="RPCI-98" /note="end : TET3"	11.0\$; Score 55; DB 29; Length 925;		1	
		57	bp	Best Local Similarity 14.8%; Pred. No. 0.001; Matches 57; Conservative 177; Mismatches 145; Indels 6; Gaps 1				
Qy		31	90	GGCCCTGGTAAGTCGCGCTGGTGGGGCAAAACCCGGACGAGCTGGACCTCCCTGGCGGC 90				
Db		539	59	KKCGGTGCGSTTTTGGYKGKGSSSCSCSCSSCCBCCCCSCS 59				
Qy		91	154	CGGCCCTCGAAATTGTCGAGACGCCGCTACTCCACCGGAGAATCACGGCCGGCTTGCT 154				
Db		599	655	YCCSSSBSSSKCSTSBCSCSSSKSVGTSCTSSSSSSSTSSTS 655				
Qy		151	214	TGCTGCGCTGTGTTACAGCGCGGTGGCTGGGGCTCTCGCAGATCGACATGTTGC 214				
Db		659	711	SGSSSSSSSSYTTSKTSASGSWSAGGGSSGTTGTTSSSSSSSTSSTSSSSSSSS 711				
Qy		211	267	TTCCTGCATCCAGAAAGATC----GTGCGGGGGGACCCGTATAAGCTGTTCTGCCGCT 267				
Db		719	771	TBSSGSBSSGSSSSSTSSBCTSTSSTSSSSSYSSSTSCTCCSYSSSTS 771				
Qy		265	324	CGAGCTCGCGTGTGGGGCACTCATGTCGGATGGCAAACGTCAGGGCGGA 324				
Db		779	833	TNGSTSGBSSSSSVGTBSSSDSTSCTSSCCCYMTCCTSYTBMBCYTSTS 833				
Qy		325	381	GATTCGTGATCGAGCTGGATCCATTGCGGGTGTGGATGTCGCCCGCTAGGGTC 381				
Db		839	891	GTRGCGCGSSGTSNGBGTSSACSSSSSSSSVSSSKSASSSSVSSSSGGVSS 891				
Qy		385	409	CATCACGCTGTCCGGGCCACCGA 409				
Db		899	923	NSSASKSSSGVSSGSGSGSV 923				
RESULT	3	BZ549462	BZ549462	812 bp	DNA	linear	GSS 17-DEC-2004	
LOCUS		pac1-60_2079.x1	pac1-60_2079	Pseudomonas aeruginosa	genomic	clone		
DEFINITION								
ACCESSION		BZ549462	BZ549462	Genomic survey sequence.				
VERSION			G1	GI:27153043				
KEYWORDS								
SOURCE								
ORGANISM								
Pseudomonas aeruginosa								
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;								
Pseudomonadaceae; Pseudomonas.								
REFERENCE			1	(bases 1 to 812)				
AUTHORS				Spencer, D.H., Raymond, C.K., Smith, B.E., Sims, E.B., Hastings, M.,				
VERSION				Burns, J.L., Kahl, R. and Olsen, M.V.				
KEYWORDS				Whole-Genome Sequence variation among multiple isolates of				
SOURCE				Pseudomonas aeruginosa library				
ORGANISM				J. Bacteriol. (2002) In press				
Pseudomonadaceae; Pseudomonas.				Contact: Chris K. Raymond				
REFERENCE				Genome Center				
AUTHORS				University of Washington				
VERSION				Box 352145, Seattle, WA 98105-2145, USA				
KEYWORDS				Tel: 206216954				
SOURCE								
ORGANISM								
Pseudomonas aeruginosa								
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;								
Pseudomonadaceae; Pseudomonas.								
REFERENCE			1	(bases 1 to 812)				
AUTHORS				Spencer, D.H., Raymond, C.K., Smith, B.E., Sims, E.B., Hastings, M.,				
VERSION				Burns, J.L., Kahl, R. and Olsen, M.V.				
KEYWORDS				Whole-Genome Sequence variation among multiple isolates of				
SOURCE				Pseudomonas aeruginosa library				
ORGANISM				J. Bacteriol. (2002) In press				
Pseudomonadaceae; Pseudomonas.				Contact: Chris K. Raymond				
REFERENCE			1	Genome Center				
AUTHORS				University of Washington				
VERSION				Box 352145, Seattle, WA 98105-2145, USA				
KEYWORDS				Tel: 206216954				

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DOM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 16:42:52 ; Search time 232 Seconds

(without alignments)
5829.390 Million cell updates/sec

Title: US-09-484-577A-3

Perfect score: 501
Sequence: 1 actctccaggctctaccgaa.....cagaatgcggatgtat 501

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

5105512

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

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RESULT

1

AT37329/C

ID AT37329 standard; DNA;

28804 BP.

AC AT37329;

XX XX

DT DT

30-NOV-1996 (first entry)

DE DE

Sphingan biosynthetic gene region.

XX XX

KW KW

XX XX

OS OS

Sphinomonas strain S88 (ATCC 31554).

PH PH

Key

CDS CDS

FT FT

CDS	complement (7076..7078)		PF 24-JAN-1996; 96EP-0300467.
	/*tag= e		XX
	/codon_start= 7076..7078		PR 24-JAN-1995; 95US-0377440.
	/note= "spst1 gene putative initiation codon"		XX
	7588..7590		(SHIN-) SHINETSU BIO INC.
	/codon_start= 7588..7590		PA (SHIE) SHINETSU CHEM CO LTD.
	/note= "spsk1 gene putative initiation codon"		XX
	8643..8645		Armentrout RW, Mikolajczak M, Pollock TJ, Thorne L;
	/tag= g		PI Yamaoka M;
	/codon_start= 8643..8645		XX
	/note= "spsl1 gene putative initiation codon"		WPI; 1996-386292/39.
	complement (10940..10940)		DR PR-PSDB; ARIW0397.
CDS	/*tag= h		XX
	/codon_start= 10938..10940		New isolated DNA from <i>Sphingomonas</i> sp. - used for transforming
	/note= "spsj1 gene putative initiation codon"		PT recipient bacteria to obtain hyper-producers of sphingan
	11569..11571		PT polysaccharide(s).
	/tag= i		XX
	/codon_start= 11569..11571		PS Claim 32; Page 56-70; 105pp; English.
	/note= "spsf1 gene putative initiation codon"		XX
	12886..12888		CC A 28.8 kb chromosomal fragment of <i>Sphingomonas</i> strain S88 was
	/tag= j		CC isolated on the basis of its ability to restore sphingan
CDS	/codon_start= 12886..12888		CC biosynthetic capability to <i>Sphingomonas</i> mutant S88m260. It
	/note= "spsd1 gene putative initiation codon"		CC contains 23-25 genes, including sps genes coding for biosynthesis of
	15165..15167		CC the polysaccharide sphingan, rns genes coding for a transport function and some
	/tag= k		CC biosynthesis, atrB genes coding for a transport function and some
CDS	/codon_start= 15165..15167		CC unidentified open translation reading frames (urf). The spsB gene
	/note= "spse1 gene putative initiation codon"		CC was identified to code for glucosyl IP-transferase
	15883..15885		CC (AAW03997), an enzyme catalyzing the first step of assembly of
	/tag= l		CC sphingan carbohydrates. DNA fragments of S88 can be inserted into
	/codon_start= 15883..15885		CC a vector in multiple copies and used to produce engineered bacteria
	/note= "urf32 gene putative initiation codon"		CC that are hyper-producers of sphingan.
	16748..16750		XX
	/tag= m		SQ Sequence 28804 BP; 4974 A; 9806 C; 9228 G; 4796 T; 0 other;
	/codon_start= 16748..16750		Query Match 17.7%; Score 88.8; DB 17; Length 28804;
	/note= "urf26 gene putative initiation codon"		Best Local Similarity 56.5%; Pred. No. 9.4e-13;
CDS	complement (21082..21084)		Mismatches 0; Mismatches 127; Indels 0; Gaps
	/tag= n		Matches 165;
	/codon_start= 21082..21084		Qy 80 TTCTTCCGGCGCCCTCGAATTTGTCGAGGCCCATCTCCACCGCAGACTACG 1
	/note= "urfr1 gene putative initiation codon"		Db 18808 TTCCCTCCGGCGCTGGCTGGATCATCGAGCTCCGGCTCAC 1
	21706..23118		Qy 140 GCCTCTTGCTGTCTTCTACTGCCTCCGCTGGCGCTGGCGGTCTGGCGAGGATC 1
	/tag= o		Db 18748 GGCGGGGTGTGGCTGGGGGGCTGGGATCAACCGCTGGCTGGCAATGGCGGTG 1
	/label= spSB		Qy 200 GACATCGTTGCTCTGCATCCAGAAAGATCTGGCTGGCTGGCTGGTAAAAGCTGGTTCAG 2
	/product= Glucosyl IP-transferase		Db 18688 GAAGTGGTGGGGCGACGAGGGCCATCGCCGAGACGAGATCGTGCAAG 1
CDS	23238..23240		Qy 260 CGCTCGAGGTGGCTGGCTGGCGCACTCATGTCGGCATGGCAAACCGTCAAGGC 3
	/tag= p		Db 18628 TCCCCGGAAAACGGPATCGTCCGGCCATTGGTGGCTGGGGAGAACGCTTCAGAAG 1
	/codon_start= 23238..23240		Qy 320 GCGGAGATTCTGATCCAGCTGGATCATTCGGGGTGGATGGTGGATGTTGCC 371
	/note= "rhsA gene putative initiation codon"		Db 18568 GCGCAGGTGTGATCAGCTCGATCCACCATGTCGGAGCCGAAGCCGCC 18517
	24113..24115		RESULT 2
	/tag= q		AAT92474/2
CDS	/codon_start= 24113..24115		ID AAT92474 standard; DNA; 28804 BP.
	/note= "rhsC gene putative initiation codon"		XX
	24683..24685		AC AAT92474;
	/tag= r		XX
	/codon_start= 24683..24685		DT 04-FEB-1998 (first entry)
	/note= "rhsB gene putative initiation codon"		XX
	25744..25746		DE <i>Sphingomonas</i> genus microbe isolated DNA sequence producing sphingan.
	/tag= s		XX
	/codon_start= 25744..25746		KW <i>Sphingomonas</i> microbe; sphingan polysaccharide biosynthesis gene;
	/note= "rhsD gene putative initiation codon"		XX
CDS	complement (27534..27536)		OS Sphingomonas sp.
	/tag= t		
	/codon_start= 27534..27536		
	/note= "urf31 gene putative initiation codon"		
	27747		
	/tag= u		
	/codon_start= 27747..27749		
	/note= "urf34 gene putative initiation codon"		
	28-AUG-1996		
EP728841-A2.			

Result No.	Score	Query	Match	Length	DB ID	Description
1	59.2	11.8	1428	11	US-09-884-696-36	Sequence 36, Appl_i
c 2	51.2	10.2	1803	14	US-10-156-761-4249	Sequence 4249, Appl_i
c 3	51.2	10.2	9025608	14	US-10-156-761-1	Sequence 1, Appl_i
c 4	43.8	8.7	819	14	US-10-156-761-4175	Sequence 4175, Appl_i
c 5	43.4	8.7	681	14	US-10-156-761-2703	Sequence 2703, Appl_i
c 6	43.4	8.7	9025608	14	US-10-156-761-1	Sequence 1, Appl_i
c 7	40.6	8.1	768	14	US-10-156-761-6013	Sequence 6013, Appl_i
c 8	40.6	8.1	1758	14	US-10-156-761-5524	Sequence 6524, Appl_i
c 9	39.4	7.9	393	14	US-10-156-761-1979	Sequence 1979, Appl_i
c 10	39	7.8	1761	10	US-09-738-626-1439	Sequence 1439, Appl_i
c 11	39	7.8	3394900	10	US-09-738-626-1	Sequence 1, Appl_i
c 12	38.4	7.7	1050	14	US-10-156-761-4467	Sequence 4467, Appl_i
c 13	38.2	7.6	1578	14	US-10-156-761-6129	Sequence 6129, Appl_i
c 14	37.8	7.5	1038	14	US-10-156-761-6667	Sequence 6667, Appl_i
c 15	37.4	7.5	2715	14	US-10-156-761-2245	Sequence 2245, Appl_i
c 16	37.2	7.4	375	10	US-09-960-352-13368	Sequence 13368, Appl_i

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

TYPE: DNA

ORGANISM: *Moraxella bovis*

FEATURE: CDS

NAME/KEY: (1)...(1425)

LOCATION: US-09-884-696-36

SEQUENCE: US-09-884-696-36

SCORE: 59.2

DB: 11

LENGTH: 1428

PRED. NO.: 5.2e-08

BEST LOCAL SIMILARITY: 49.1t

PRED. NO.: 41

NUMBER OF SEQ ID NOS: 163

TITLE OF INVENTION: MORAXELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 36

TITLE OF INVENTION: BOVIS INFECTIONS

FILE REFERENCE: 481_06

CURRENT APPLICATION NUMBER: US-09-884-696

CURRENT FILING DATE: 2001-06-19

SOFTWARE:

RESULT 2
US-10-156-761-4249/C
; Sequence 4249, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHITUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitillis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 10.2%; Score 51.2; DB 14; Length 9025608;
Best Local Similarity 69.4%; Pred. No. 3.9e-05;
Matches 100; Conservative 0; Mismatches 38; Indels 6; Gaps 2;

Qy 333 TCGAGCTGGAATCATTCGCGCTGGTGTGAAATGTCGCGCCGCATCGATCAGTCATCGCGCTGGTGTGATGTT 367
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Qy 392 GTGTCGCCGCCACCGATGCCACCATCTTCGACCTTCTCACCGG-----A 446
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; Sequence 4175, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROYOSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHITUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4175
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Streptomyces avermitillis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (1803)

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Best Local Similarity 69.4%; Pred. No. 2.4e-05;
Matches 100; Conservative 0; Mismatches 38; Indels 6; Gaps 2;

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Qy 392 GTGTCGCCGCCACCGATGCCACCATCTTCGACCTTCTCACCGACG-----A 446
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Qy 447 GTCACCCCCGAGTTGCCGATAATG 470
Db 644 GTGACCCGGAGTTGCCGATGTTG 621

RESULT 3
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROYOSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHITUKI

Qy 62 ACCGGGAGGAGCTGGCCCTCTCGCGGCCGCCCTCGAAATGTCGAGACGGCCATCT 121

Query Match 8.7%; Score 43.8; DB 14; Length 819;
Best Local Similarity 45.9%; Pred. No. 0.002e-01;
Matches 150; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Result No.	Score	Query	Match	Length	DB ID	Description
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C 2	88.8	17.7	28804	3	US-09-096-942-2	Sequence 2, Appli
C 3	88.8	17.7	28804	3	US-09-096-867-2	Sequence 2, Appli
C 4	51.6	10.3	5120	3	US-08-772-270A-6	Sequence 6, Appli
C 5	51.6	10.3	8310	2	US-08-488-706-1	Sequence 1, Appli
C 6	51.6	10.3	8310	4	US-09-062-126-1	Sequence 1, Appli
C 7	9.6	13.8	80	4	US-09-252-991A-3550	Sequence 3550, Ap
C 8	48	9.6	1947	4	US-09-252-991A-3557	Sequence 3557, Ap
C 9	47.6	9.5	1608	4	US-09-252-991A-1154	Sequence 11655, A
C 10	47.6	9.5	1608	4	US-09-252-991A-1165	Sequence 11769, A
C 11	47.6	9.5	1608	4	US-09-252-991A-1169	Sequence 11769, A
C 12	47	9.4	4403765	3	US-09-103-840A-2	Sequence 1, Appli
C 13	47	9.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 14	42	9.4	4403725	3	US-09-103-840A-2	Sequence 1, Appli
C 15	42	8.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 16	40.6	8.1	1572	4	US-09-252-991A-3270	Sequence 3270, Ap
C 17	40.6	8.1	1965	4	US-09-252-991A-3234	Sequence 3234, Ap
C 18	40.6	8.1	2325	4	US-09-252-991A-3413	Sequence 3413, Ap
C 19	40.2	8.0	822	4	US-09-252-991A-9029	Sequence 9029, Ap
C 20	40.2	8.0	1527	4	US-09-252-991A-8978	Sequence 8978, Ap
C 21	40.2	8.0	2043	4	US-09-252-991A-8759	Sequence 16314, A
C 22	39.2	7.8	2034	4	US-09-252-991A-16314	Sequence 15964, A
C 23	39.2	7.8	2190	4	US-09-252-991A-15964	Sequence 15964, A
C 24	39	7.8	1254	4	US-09-252-991A-4072	Sequence 4072, Ap
C 25	39	7.8	1404	4	US-09-252-991A-4118	Sequence 4118, Ap
C 26	39	7.8	1680	4	US-09-252-991A-4087	Sequence 4087, Ap
C 27	38.4	7.7	435	4	US-09-252-991A-81	Sequence 81, Appli

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:
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 3: /cgns2_6/pctodata/1/ina/6A_COMB.seq:
 4: /cgns2_6/pctodata/1/ina/6B_COMB.seq:
 5: /cgns2_6/pctodata/1/ina/PCITS_COMBO.seq:
 6: /cgns2_6/pctodata/1/ina/backtles1.seq:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
 US-08-592-874-1/C
 ; Sequence 1, Application US/08592874
 ; Patent No. 5854034
 ; GENERAL INFORMATION:
 ; APPLICANT: POLLACK, THOMAS J.
 ; APPLICANT: YAMAZAKI, MOTOHIDE
 ; APPLICANT: THORNE, LINDA
 ; APPLICANT: MIKOLAJCZAK, MARCIA
 ; APPLICANT: ARMENTROUT, RICHARD W.
 ; TITLE OF INVENTION: DNA SEGMENTS AND METHODS FOR INCREASING NUMBER OF SEQUENCES: 1
 ; TITLE OF INVENTION: POLYSACCHARIDE PRODUCTION
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: JULES E. GOLDBERG
 ; STREET: 261 MADISON AVENUE
 ; CITY: NEW YORK
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10016-2391

%

Description

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/592,874
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/377,440
 FILING DATE: 24-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: GOLDBERG, JULES E.
 REGISTRATION NUMBER: 24,408
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-986-4090
 FAX: 212-818-9479
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28804 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 FRAGMENT TYPE: N-terminal
 US-08-592-874-1

Query Match Score 88.8; DB 2;
 Best Local Similarity 56.5%; Pred. No. 2.7e-14;

Matches 165; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
 Query 80 TTCTCGCCGGCCCTGAAATGTGAGACGCCATCCACGGCAAGTCACG 139
 Database 18808 TTCTCGCCGGCCCTGAAATGTGAGACGCCATCCACGGCAAGTCACG 18749
 Query 140 GCGCCTTGTGCTTGCTTGCTTGTCTACTCGCCCTGGCTGGCTGGCTAAC 199
 Database 18748 GCGGGTTGATGGTGAGGGCTGGCATACACCGCTGGGTG 18689
 Query 200 GACAICGTTGCTTGATGGCTCATCGAAAGATCTGCGGGGACCGTAAAGCTGGTCAAGTCAG 259
 Database 18688 GAAGTGGTGCCTGGCCACGGCGCATGGCGAGAACAGATGTCAG 18629
 Query 260 CGCTCGAGTGGCTGGCTGGCTGGCCATCTGTCGGGATGAAACCTGAGGCC 313
 Database 18628 TCCCCGAAAGGGTATGCTGGGGCATTCGTGGCGAGGAAGTCGAAG 18569
 Query 320 GGCGGATTCTGATCAGTGGATGATCGCTGGATGTTGGATGTTGCC 371
 Database 18568 GCGCGGTGCTGATCAGCTGGATGCCACATGCGGAGCGCGC 18517

RESULT 2
 US-09-096-942-2/C
 ; Sequence 2, Application US/09096942
 ; Patent No. 6027925
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollock, Thomas J
 ; APPLICANT: Mikolajczak, Marcia
 ; APPLICANT: Yamazaki, Motohide
 ; APPLICANT: Thorne, Linda
 ; APPLICANT: Armentrout, Richard W
 ; TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria
 ; TITLE OF INVENTION: Carrying Genes from Xanthomonas Campestris
 ; FILE REFERENCE: seq list for appl filed from pro. appl
 ; CURRENT APPLICATION NUMBER: US/09/096,942
 ; CURRENT FILING DATE: 1998-06-12
 ; EARLIER FILING DATE: 1997-06-12
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.0
 ; LENGTH: 28604
 ; TYPE: DNA
 ; ORGANISM: Sphingomonas sp. S88
 ; SEQ ID NO: 2
 ; LENGTH: 28804
 ; TYPE: DNA
 ; ORGANISM: Sphingomonas sp. S88
 ; SEQ ID NO: 2
 ; LENGTH: 28804

RESULT 3
 JS-09-096-867-2/C
 ; Sequence 3, Application US/09096867
 ; Patent No. 6030817
 ; GENERAL INFORMATION:
 ; APPLICANT: Pollock, Thomas J
 ; APPLICANT: Mikolajczak, Marcia
 ; APPLICANT: Yamazaki, Motohide
 ; APPLICANT: Thorne, Linda
 ; APPLICANT: Armentrout, Richard W
 ; TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria
 ; TITLE OF INVENTION: Carrying Genes from Xanthomonas Campestris
 ; FILE REFERENCE: seq list for appl filed from pro. appl
 ; CURRENT APPLICATION NUMBER: US/09/096,867
 ; CURRENT FILING DATE: 1998-06-11
 ; EARLIER APPLICATION NUMBER: 60/049,428
 ; EARLIER FILING DATE: 1997-06-12
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 2
 ; LENGTH: 28804
 ; TYPE: DNA
 ; ORGANISM: Sphingomonas sp. S88
 ; SEQ ID NO: 2
 ; LENGTH: 28804;
 ; Best Local Similarity 56.5%; Pred. No. 2.7e-14; Indels 0; Gaps 0;
 ; Matches 165; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
 ; Best Local Similarity 56.5%; Pred. No. 2.7e-14; Indels 0; Gaps 0;
 ; Matches 165; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
 ; Qy 80 TTCTCGCCGGCCCTGAAATGTGAGACGCCATCCACGGCAAGTCACG 139
 ; Db 18808 TTCTCGCCGGCCCTGAAATGTGAGACGCCATCCACGGCAAGTCACG 18749
 ; Qy 140 GCGCCTTGTGCTTGCTTGCTTGTCTACTCGCCCTGGCTGGCTAAC 199
 ; Db 18748 GCGGGTTGATGGTGAGGGCTGGCATACACCGCTGGGTG 18689
 ; Qy 200 GACAICGTTGCTTGATGGCTCATCGAAAGATCTGCGGGGACCGTAAAGCTGGTCAAGTCAG 259
 ; Db 18688 GAAGTGGTGCCTGGCCACGGCTGGCATTCGTGGGACTATGTCGGGATGCAACCTGCAAGTCAG 18629
 ; Qy 260 CGCTCGAGTGGCTGGCTGGCTGGCCATCTGTCGGGACTATGTCGGGATGCAACCTGCAAGTCAGGCC 313
 ; Db 18628 TCCCCGAAAGGGTATGCTGGGGCATTCGTGGCGAGGAAGTCGAAG 18569
 ; Qy 320 GGCGGATTCTGATCAGTGGATGATCGCTGGATGTTGGATGTTGCC 371
 ; Db 18568 GCGCGGTGCTGATCAGCTGGATGCCACATGCGGAGCGCGC 18517

RESULT 4
 US-09-096-942-2/C
 ; Sequence 4, Application US/09096942
 ; Patent No. 6019384
 ; GENERAL INFORMATION:
 ; APPLICANT: MacInnes, Janet
 ; APPLICANT: Ricciatti, Paul
 ; APPLICANT: Mallard, Bonnie
 ; APPLICANT: Rosenda, Soren
 ; APPLICANT: Beeskow & Parr
 ; STREET: 40 King Street West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5H 3Y2
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

GenCore version 5.1.6
 Copyright (C) 1993 - 2003 Compagen Ltd.

Om: protein - nucleic search, using frame_Plus_P2n model

Run on: October 23, 2003, 11:14:15 ; Search time 2864 Seconds
 (without alignments)
 1771.227 Million cell updates/sec

Title: US-09-484-577A-4
 Perfect score: 6/68
 Sequence: 1 LSSLSPRMKSAREVVAVGGK.KAGEILIELDPAGGYDVAT 124

Scoring table: BL053M62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delect 7.0

Searched: 288711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+P2n.model -DBV=xjh
-Q=/cgn2.1/uspt0/spool/US99484577/runat_23102003_111410_17988/app_query.fasta_1.263
-D=GeneBnd1 -QFNM=fascap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPTR=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human0.cdi -LIST=45
-DOCALLIGN=0 -THR SCORE=0.01 -THR MAX=100 -THR MIN=0 -ALIGNN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-NO_MMAP -LARGEQT -CGN 1 -NCPU=6 -ICPU=3
-USER=US99484577 @CGN 1 -NCPU=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELECT=7
```

Gen:Emb1 :

Database :

```
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_to:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_tun:*
17: em_hum:*
18: em_in:*
19: em_md:*
20: em_on:*
21: em_or:*
22: em_ov:*
23: em_pt:*
24: em_ph:*
25: em_pi:*
26: em_ro:*
27: em_sts:*
28: em_un:*
```

29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pnt:*
35: em_hg_rdt:*
36: em_hg_mam:*
37: em_hg_vrt:*
38: em_sy:*
39: em_hg_o_hum:*
40: em_hg_o_mus:*
41: em_hg_o_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Result No.						Query Score	Match Length	DB ID	Description
C	1	312	51.3	30650	1	AB005958	Bradyrhiz	AB011858	Xanthomon
C	2	246	40.5	10902	1	AE013811	AE013811	AE013811	Yersinia
C	3	243	40.0	11180	1	AJ414151	AJ414151	AJ414151	Xylella f
C	4	243	40.0	334050	1	AE004049	AE004049	AE004049	Xylella f
C	5	241	39.6	11552	1	AE012558	AE012558	AE012558	Xylella f
C	6	239	39.3	30222	1	NM391263	NM391263	NM391263	Neisseria
C	7	238	39.1	1428	1	AE012172	AE012172	AE012172	Neisseria
C	8	238	39.1	4254	1	AF121772	AF121772	AF121772	Neisseria
C	9	238	39.1	11381	1	AE002524	AE002524	AE002524	Neisseria
C	10	238	39.1	34980	6	AX044033	AX044033	AX044033	Sequence
C	11	238	39.1	34980	6	AY044034	AY044034	AY044034	Sequence
C	12	235	38.7	7324	1	NM391260	NM391260	NM391260	Neisseria
C	13	235	38.7	32601	1	NM622491	NM622491	NM622491	Neisseria
C	14	231	38.1	301708	1	AE016792	AE016792	AE016792	Pseudomon
C	15	218	35.9	189050	1	AL646077	AL646077	AL646077	Ralstonia
C	16	215	35.4	28804	1	SS051197	SS051197	SS051197	Springomon
C	17	215	35.4	28804	1	AR068625	AR068625	AR068625	Sequence
C	18	205	33.7	3326	1	AF273216	AF273216	AF273216	Rhizobium
C	19	182	29.9	6752	1	AF314503	AF314503	AF314503	Mannheimi
C	20	182	29.9	6932	1	AF314505	AF314505	AF314505	Mannheimi
C	21	182	29.9	6952	1	AF314508	AF314508	AF314508	Mannheimi
C	22	182	29.9	6952	1	AF314509	AF314509	AF314509	Mannheimi
C	23	182	29.9	6952	1	AF314510	AF314510	AF314510	Mannheimi
C	24	182	29.9	6952	1	AF314512	AF314512	AF314512	Mannheimi
C	25	182	29.9	6952	1	AF314514	AF314514	AF314514	Mannheimi
C	26	182	29.9	6952	1	AF314515	AF314515	AF314515	Mannheimi
C	27	182	29.9	6952	1	AF314516	AF314516	AF314516	Mannheimi
C	28	182	29.9	6952	1	AF314517	AF314517	AF314517	Mannheimi
C	29	182	29.9	6952	1	AF314523	AF314523	AF314523	Pasteurel
C	30	182	29.9	6952	1	AF314524	AF314524	AF314524	Pasteurel
C	31	182	29.9	6958	1	AF314524	AF314524	AF314524	Pasteurel
C	32	182	29.9	6958	1	AF314526	AF314526	AF314526	Pasteurel
C	33	182	29.9	7742	1	PSLTKTCABD	PSLTKTCABD	PSLTKTCABD	M24197
C	34	181	29.8	6669	1	AF314521	AF314521	AF314521	P haemo lytic
C	35	181	29.8	6955	1	AF314513	AF314513	AF314513	Mannheimi
C	36	181	29.8	6952	1	AF314523	AF314523	AF314523	Pasteurel
C	37	181	29.8	6952	1	AF314519	AF314519	AF314519	Mannheimi
C	38	181	29.8	6952	1	AF314520	AF314520	AF314520	Mannheimi
C	39	181	29.8	6952	1	AF314522	AF314522	AF314522	Mannheimi
C	40	181	29.8	300883	1	AB016809	AB016809	AB016809	Vibrio vu
C	41	179	29.4	7801	1	PSAIIKCT	PSAIIKCT	PSAIIKCT	M20730
C	42	179	29.4	7641	1	PABLURKT	PABLURKT	PABLURKT	L12148
C	43	177	29.1	7489	1	PAU66588	PAU66588	PAU66588	Pasteurella
C	44	177	29.1	7773	1	AF3B1184	AF3B1184	AF3B1184	Actinobac
C	45	176	28.9	15746	1	X80055	X80055	X80055	A. pleurope

ALIGNMENTS

RESULT 1

AP005958/c
LOCUS AP005958
DEFINITION Bradyrhizobium japonicum USDA 110 DNA, complete genome, section 24/31
ACCESSION AP005958
VERSION BA000040
KEYWORDS AP005958.1 GI:27354550
SOURCE Bradyrhizobium japonicum USDA 110
ORGANISM Bradyrhizobium japonicum USDA 110
BACTERIA: Proteobacteria; Alpha proteobacteria; Rhizobiales;
 Bradyrhizobiaceae; Bradyrhizobium.

REFERENCE Kaneko,T., Nakamura,Y., Sato,S., Minamisawa,K., Uchiumi,T., Sasamoto,S., Watanabe,A., Idesawa,K., Iiguchi,M., Kawashima,K., Kohara,M., Matsunoto,M., Shimpo,S., Tsuruoka,H., Wada,T., Yamada,M., and Tabata,S.

AUTHORS Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110 (supplement)

TITLE DNA Res. 9 (6), 189-197 (2002)

JOURNAL MEDLINE
PUBMED 12597275

REFERENCE 2
AUTHORS Kaneko,T., Nakamura,Y., Sato,S., Minamisawa,K., Uchiumi,T., Sasamoto,S., Watanabe,A., Idesawa,K., Iiguchi,M., Kawashima,K., Kohara,M., Matsunoto,M., Shimpo,S., Tsuruoka,H., Wada,T., Yamada,M., and Tabata,S.

TITLE Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110 (supplement)

JOURNAL DNA Res. 9 (6), 225-256 (2002)

MEDLINE URL: http://www.kazusa.or.jp/rhizobase/
PUBMED Tel: 81-438-52-3935 (ex. 2338), Fax: 81-438-52-3934)
PUBLISHER Location/Qualifiers 1..302650

FEATURES Source
product "transcriptional regulatory protein"
protein_id "BAC51537.1"
db_xref "GI:27354551"
translation "MENIILESSSEVSESSGUGLPLVANSGRGDMAMFTDLOAFAWID LQEPRDHQLRQAQAPRERWRRLDRGPEAIIETTSRWEDEDSHSDATPD RTFVGIAALKATPAKTDIDRQVFLRDFLAELARALTEHGDAADEFTCVCQTLAME: ARRE PPARVNLPKRBLPRVEQYADNFCISSELANAVSLRMHFAQPRATGYRPR EYLINHRIBAKTLLATGTPRLAE: ALAVGSTOAHSTVKRISGOSPARWLASKA EPILAAEALPFRRAEADMMAAAA"

complement (1428..3794)
gene "B116273"
complement (1428..3794)
gene "B116273"
note "ORF ID:b116273 probable biotin sulfoxide reductase"

codon_start 1
transl_table 11
protein_id "BAC51538.1"

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ON protein - nucleic search, using frame_plus_P2n model

Run on: October 23, 2003, 11:14:20 ; Search time 1724 Seconds

(without alignments)
1748.118 Million cell updates/sec

Title: US-09-484-577A-4

Perfect score: 608

Sequence: I LSSLSPRMKSMAREVVAVGGK. KAGEILIELDPFAGGVDVAT 124

Scoring table: BLOSUM62

Xgapop 10.0 Xgapext 0.5

Ygapop 10.0 Ygapext 0.5

Fgapop 6.0 Fgapext 7.0

Delop 6.0 Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+P2n,model -DEV=x1h

-O=/cgn2_1/USP0/spool/US09484577/runat_23102003_111410_18001/app_query.fasta_1..263

-DB=EST -QFORMAT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPCLIP=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=humaro40_cdi -L=ST=45

-DOCALIGNN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGNN=15 -MODE=LOCAL

OUTFILE=pt0 -NORM=exc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

USER=US09484577 @runat_1.1 -NEGS COPE=0 -WAIT -DESBLOCK=100 -LONGLOG

NO MMAP -LARGEQUERY -NEGS COPE=0 -WAIT -DESBLOCK=100 -LONGLOG

DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6

FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELPOP=6 -DELEXT=7

)atabase : EST :

1: em_estba:*

2: em_estch:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_num:*

18: em_gss_inv:*

19: em_gss_pnt:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mut:*

24: em_gss_pro:*

25: em_gss_rct:*

26: em_gss_pig:*

27: em_gss_vrt:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
C 1	122	20.1	772	AF075872	AF075872 AF075872
C 2	117	19.2	1126	29	BZ573090 msh2 2939
C 3	105	17.3	750	28	AF075852 AF075852
C 4	95.5	15.7	945	28	BZ54254 BZ54254
C 5	92	15.1	812	29	BZ549462 BZ549462
C 6	87	14.3	961	10	BF781847 BF781847
C 7	85.5	14.1	455	10	Leishmania
C 8	85	14.0	682	29	AG163349 Pan trogl
C 9	84	13.8	432	10	WHE2231 G
C 10	84	13.8	756	28	AQ99116 REC0179F
C 11	83.5	13.7	610	12	BM631476 170006875
C 12	83.5	13.7	973	20	BG758550 602711239
C 13	83	13.7	939	20	BZ706228 PUBLISTTD
C 14	82.5	13.6	431	29	B288303 CH240_241
C 15	82.5	13.6	1175	29	BZ58366 Pacs1_60
C 16	82	13.5	456	12	BJ189099 BJ189099
C 17	82	13.5	884	29	BZ636906 OGCK65TM
C 18	81.5	13.4	563	18	BH775270 fimb011f0
C 19	81.5	13.4	678	14	CD425333 SA1_11_H0
C 20	81	13.3	463	9	AU070712 AU070712
C 21	81	13.3	906	14	CB575007 AGENCOURT
C 22	80	13.2	795	29	AL348149 AGENCOURT
C 23	80	13.2	1201	9	AL514080 AL514080
C 24	80	13.2	1337	29	BZ572552 msh2_3874
C 25	79.5	13.1	360	10	BE48113 167524 BA
C 26	79.5	13.1	394	14	D27997 CEUK007EF
C 27	79.5	13.1	423	9	AI969333 wipf6h04_X
C 28	79.5	13.1	507	13	BQ606308 BRY 2784
C 29	79.5	13.1	532	13	BQ817896 1030066H0
C 30	79.5	13.1	768	12	BI908989 603070521
C 31	79.5	13.1	1002	13	BX344531 BX344531
C 32	79.5	13.1	1088	29	BZ577884 msh2_5430
C 33	79	13.0	487	10	BG158865 RHI22_4
C 34	79	13.0	710	12	BJ570919 BJ570919
C 35	79	13.0	711	12	BZ568037 BJ568037
C 36	79	13.0	946	10	BF305164 601892608
C 37	79	13.0	969	10	BF787122 602105661
C 38	79	13.0	1159	14	AG071759 Pan trogl
C 39	78.5	12.9	499	14	CA621031 wlin_pk00
C 40	78.5	12.9	528	14	CB99305 AGENCOURT
C 41	78.5	12.9	734	28	BZ577887 msh2_5621
C 42	78.5	12.9	775	29	BZ577887 msh2_5621
C 43	78.5	12.9	825	12	BI603588 603247491
C 44	78.5	12.9	852	29	BZ553772 pacsl_60
C 45	78.5	12.9	853	29	CC115510 NDL71C2_

ALIGNMENTS

RESULT 1	AF075872/c	GSS 29-AUG-2000
LOCUS	AF075872	Salmonella typhimurium LT2, Lambda DASH II Salmonella
DEFINITION	typhimurium Genomic clone 142-T3,	genomic survey sequence.
ACCESSION	AF075872	
VERSION	AF075872.1	GI:3320742
KEYWORDS		GSS.
ORGANISM	Salmonella typhimurium	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
SOURCE	Salmonella typhimurium	Enterobacteriaceae; Salmonella.
REFERENCE	1 (bases 1 to 772)	1 (bases 1 to 772)

AUTHORS Wong, R.M.-Y., Wong, K.K., Benson, N.R. and McClelland, M.
TITLE Sample sequencing of a *Salmonella typhimurium* LT2 lambda library:
 comparison to the *Escherichia coli* K12 genome
JOURNAL *FEBS Microbiol. Lett.* 173 (2), 411-423 (1999)
PUBMED 99243757
LINK [10227170](http://pubmed.ncbi.nlm.nih.gov/99243757/)
COMMENT Contact: McClelland M
 Molecular Biology
 Sidney Kimmel Cancer Center
 3099 Science Park Road, San Diego, CA 92121, USA
 Email: mclelland@ifsci.sdsu.edu
NUCLEOTIDES Class: shotgun
 Location/Qualifiers
 1. .772
 /organism="Salmonella typhimurium"
 /mol_type="genomic DNA"
 /strain="LT2"
 /db_xref="ITaxon: 602"
 /clone="142-T3"
 /clone_id="Salmonella typhimurium LT2, Lambda DASH II"
 /note="Vector: Lambda DASH II; sequenced using Li-Cor
 sequencer"
SEQUENCE SE COUNT 169 a 229 c 205 g 167 t 2 others
PROTEINS IGIN
SOURCE
ALIGNMENT Scores:
 ed. No.: 0.00187 Length: 772
 score: 122.00 Matches: 26
 percent Similarity: 61.11% Conservative: 18
 st Local Similarity: 36.11% Mismatches: 28
 Every Match: 20.07% Indels: 1
 :.: Gaps: 0
 -09-484-577A-4 (1-124) x AF075872 (1-772)
 49 LeuLeuAlaAlaLeuLeuPhsTyrCysAlaValAlaTTpAlaGlyLeuGlyArgIleAspIle 68
 ::::: ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 336 ATCTGGCTCACTGATTTCTCATTCCTCGCGCATCTGGCGTGTCTGGCCGACTGGATGAG 27
 69 valValaserLaserArgLysIlevalProGlyAspArgVallysLeuValGlnProLeu 88
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 276 GTTTCACCGCCACGGAAAGTGATCCCACTGAGTCTGCAGTCAGGTAACAGGTTCTGCAGTCGCTG 21
 89 GluValGlyValValArgAlaThrHisValArgAspGlyGlnThrVallysAlaGlyGlu 10
 ::::: ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 216 GATGGCGCATTCGGCCAGTGAACGTTGACGTGCGGAAGCGACAGATTCAGCTAACCG 15
 109 IleLeuIleGluLeuAspProHeAlaGlyGlyVal 120
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 156 ATTGTGCCGGCTGATCCGAC-GCCTCTGGCTC 122

RESULT 2
LOCUS B2573090/c 1126 bp DNA linear GSS 17-DEC-20
DEFINITION msh2, Y2 msh *Pseudomonas aeruginosa* genomic clone mst2_2939.
VERSION B2573090 1
ACCESSION B2573090_1 GI:27208151
KEYWORDS
ORGANISM *Pseudomonas aeruginosa*
Pseudomonas aeruginosa
 Bacteria: Proteobacteria: Gammaproteobacteria: Pseudomonadales;
Pseudomonadaceae: Pseudomonas.
 1. (bases 1 to 126)

REFERENCE Spender, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
AUTHORS Burns, J.L., Kaul, R. and Olsen, M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
 J. Bacteriol. (2002). In press
COMMENT Contact: Chris K. Raymond
 Genome Center
 University of Washington
 Box 35145, Seattle, WA 98105-2145, USA

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and is derived by analysis of the total score distribution.

SUMMARIES							
	Query No.	Score	Match	Length	DB	ID	Description
Run on:	October 23, 2003, 11:14:14 ; Search time 236 Seconds (without alignments)	1	238	39.1	1428	21	AAT254335 Neisseria meningitidis pa
Title:	US-09-484-S7A-4	2	238	39.1	24158	21	AAQ81532 N. meningitidis pa
Perfect score:	608	3	238	39.1	34980	21	AAP21611 Neisseria meningitidis pa
Sequence:	1 LSSLSPRMRKSAREVVAVGGK.KAGEILIEFLDPPAGGYDVAT 124	4	238	39.1	34980	21	AAP21612 N. meningitidis pa
Scoring table:	BLOSUM62	5	238	39.1	837096	21	AAQ81489 Neisseria meningitidis pa
Xgapop 10.0 , Xgapext 0.5	Xgapop 10.0 , Xgapext 0.5	6	235	38.7	1305	21	AAT254336 Sphingomonas genus
Ygapop 10.0 , Ygapext 0.5	Ygapop 10.0 , Ygapext 0.5	7	215	38.4	28804	17	AAT7329 Sphingomonas S88
Fgapop 6.0 , Fgapext 7.0	Fgapop 6.0 , Fgapext 7.0	8	215	35.4	28804	18	AAT732474 Chromosomal frame
Dgapop 6.0 , Delett 7.0	Dgapop 6.0 , Delett 7.0	9	215	35.4	28804	20	AAT99812 Gene of Pasteu
Searched:	2552756 seqs, 1349719017 residues	10	215	35.4	28804	20	AAT81474 Sequence encoding
Total number of hits satisfying chosen parameters:	5105512	11	190	31.2	7184	15	E. coli CFT073 gen
Minimum DB seq length: 0		12	182	29.9	7183	11	AAC06074 ApIXBD gene. Acti
Maximum DB seq length: 2000000000		13	176	28.9	76804	24	ApxIIABCDD gene.
Post-processing: Minimum Match 0%		14	169	27.8	5120	18	A. pleuropneumonia
Post-processing: Maximum Match 100%		15	169	27.8	5120	21	ApxIIABCDD gene.
Listing first 45 summaries		16	168	27.6	7721	18	A. pleuropneumonia
Command line parameters:		17	168	27.6	7721	21	E. coli J56 pathog
-MODEL=frame+p2n model -DEV=xhl		18	154	25.3	3576	19	Escherichia coli p
-Q=cg_2.1 /USP0 spoil /US948457?/runat_23102003_1111409_17977/app_query.fasta_1..263		19	124.5	20.5	49012	24	P. coli CFT073 gen
-DB=N GenSeq 19Jun03 -QMMT=astap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0		20	124.5	20.5	49012	24	Escherichia coli p
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS:human40.cdi		21	124.5	20.5	48254	22	Escherichia coli p
-LIST=45 -DOCALLIGN=200 -THR SCORE=pc -THR MAX=100 -THR MIN=0 -ALIGN=15		22	124.5	20.5	48345	22	Pseudomonas fluorescens
-MODE=LOCAL -OUTFM=pfo -NORM=exc -HAPSIZEx=500 -MINLEN=0 -MAXLEN=300000		23	104	17.1	6400	20	Esteras's seeretary
-USER=US0203_1.1 @runat_23102003_1111409_17977 -NCPU=6 -ICPU=3		24	93	16.3	4466	17	Human DNA sequence
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG		25	90.5	15.0	2382	24	DNA encoding hydro
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -TREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6		26	90.5	14.9	9320	22	ABC transporter T1
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7		27	90	14.8	1302	23	ABC transporter
Database :	N_Geneseq_18Jun03.*	28	90	14.8	8580	23	ABU41686
1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT		29	89	14.6	5660	20	ABC transporter
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT		30	88	14.5	834	23	Pseudomonas fluore
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT		31	88	14.5	2834	23	Drosophila melanog
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT		32	88	14.5	13518	20	Drosophila melanog
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT		33	87.5	14.4	4403765	22	Mycobacterium tube
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT		34	87.5	14.4	4411529	22	Mycobacterium tube
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT		35	86	14.1	11308	23	Propionibacterium
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT		36	81.5	13.4	1395	22	E. coli proliferat
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT		37	81.5	13.4	1395	22	E. coli growth and
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT		38	81.5	13.4	2310	23	DNA encoding novel
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT		39	80.5	13.2	4362	22	Bacillus subtilis
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT		40	80.5	13.2	4540	24	Rat sequence diffe
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT		41	79	13.0	19053	21	Nucleotide sequenc
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT		42	78.5	12.9	1357	24	Human ORF8
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT		43	78.5	12.9	12772	24	Human ORF8 polynuc
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT		44	78	12.8	6848	22	Human immune/haema
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT		45	77.5	12.7	2556	25	N. gonorrhoeae muc
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT							ALIGNMENTS
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT							RESULT 1
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT							AAZ54335 standard; DNA: 1428 BP.
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT							XX
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2001.DAT							AC
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT							XX
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT							DT 21-MAR-2000 (first entry)
25: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT							XX
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							De Neisseria meningitidis ORF 764 partial DNA sequence SEQ ID NC:2619.
							KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
							KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia; antibiotic; gene therapy; ds.
							OS Neisseria meningitidis.
							PN WO9957280-A2.

XX	PD	334 GACGGGAGATGTGAAACGGGAAA CGCTGGAACTGGAGGTGTGGAAACGAC 393
XX	PF	9940-US09346.
XX	PR	01-MAY-1998; 98US-0083758.
PR	02-SEP-1998; 98US-004869.	
PR	02-SEP-1998; 98US-008994.	
PR	02-SEP-1998; 98US-009062.	
PR	09-OCT-1998; 98US-0103749.	
PR	09-OCT-1998; 98US-0103794.	
PR	09-OCT-1998; 98US-0103796.	
PR	25-FEB-1999; 99US-0121528.	
XX	PA	(CHIR) CHIRON CORP. (GENC-) INST GENOMIC RES.
XX	PI	Fraser C, Galeotti C, Grandi G, Hickey E, Massignani V, Mora M, Petersen J, Pizza M, Rappoilo R, Ratti G, Scalato E, Scarselli M;
PI	PI	Tettelin H, Venter JC;
XX	DR	WPI: 2000-062150/05.
XX	DR	P-PSDB; AAY75573.
PT	PT	Novel Neisseria polypeptides predicted to be useful antigens for vaccines and diagnostics -
PT	PS	Claim 7; Page 1243; 1453pp; English.
XX	CC	AAZ53015 to AAZ54516, AAZ54577 to AAZ54615, and AA74253 to AA75941 represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides and peptides. AAZ54337 to AAZ54576 and AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibiotics and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisseria bacteria (e.g. meningitis and septicemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
CC	Sequence 1428 BP; 341 A; 322 C; 470 G; 295 T; 0 other;	
CC	Alignment Scores:	
Qy	20 LysThrArgAspGluLeuAlaPheLeuProAlaLysLeuGluIleValGlutnProPro 39	
Score	4.8E-18	
Percent Similarity:	238.00	
Best Local Similarity:	62.14%	
Query Match:	49.51%	
D8:	39.14%	
Length:	1428	
Matches:	51	
Conservative:	13	
Mismatches:	39	
Indels:	0	
Gaps:	0	
DB	94 CGCACGGCGGAGAGCAGGGCTTTGCCGCGCATTCGAACTGAGCGGCCTC 153	
2y	40 SerProThrAlaArgLeuThrAlaAlaLeuLeuAlaLeuLeuThrCysAlaValAla 59	
DB	154 TCTGGCGCTCGAAATGGGGCGCCGTTTATATGGCTTCTGGCTTGGCTTGTTG 213	
2y	60 TrpAlaGlyLeuGlyArgIleAspIleValAlaSerAlaSerArgLysIleValProGly 79	
DB	214 TGTCTCGTGGCAAATGATATTGGCGAACGGCTGGCTGCGGC 273	
2y	80 AspArgValAlaLeuValGlnProLeuGluValGlyValAlaLysIleLeuAsp 99	
DB	274 GGCGCAAAACCACTCAAGCGCTGAAACGGCGTGTAGCTGGCGTACTGTCGGC 333	
2y	100 AspGlyGlnThrValLysAlaGlyGluIleLeuIleGluLeuAspProLeuAlaGlyGly 119	

GenCore version 5.1.6
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ON Protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 12:11:35 ; Search time 234 Seconds

(without alignments)
1421.125 Million cell updates/sec

Title: US-09-484-577A-4

Perfect score: 608

Sequence: 1 LSSLSPRMKSAREVVAVGGK.....KAGELIELDPFAGGVDVAT 124

Scoring table: BLOSUM62

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Ygapop 10.0 Ygapext 0.5
Fgapop 6.0 Fgapext 7.0
Delop 6.0 Delext 7.0

Searched: 172395 seqs, 134090051 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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LCOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
TRANS=human40_cci -LIST=5 -DOALIGN=200 -THR SCORE=pct -THR MAX=1.0C
THR MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=pro -NORMFMT=ext -HEAPSIZE=500 -MINLEN=0
MAXLEN=2000000000 -ICPU=3 -NO_MMAPP -GRUNAT=1.285 @runat_23102003_111412_18082
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LONGLOG -DV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPBLOCK=100 -XGAPEXT=0.5
FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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atabase : Published_Applications_NA:*

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4: /cgn2_6_ptodata/1/pubpna/US16_PUBCOMB.seq:*
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10: /cgn2_6_ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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12: /cgn2_6_ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6_ptodata/1/pubpna/US10B_PUBCOMB.seq:*
14: /cgn2_6_ptodata/1/pubpna/US10 NEW_PUB.seq:*
15: /cgn2_6_ptodata/1/pubpna/US60_NEW_PUB.seq:*
16: /cgn2_6_ptodata/1/pubpna/US60_PUBCOMB.seq:*
17: /cgn2_6_ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result NO.	Score	Match Length	DB ID	Description	Sequence 36, App
1	242	39.8	1428	11	US-09-884-696-36

RESULT : JS-09-884-696-36
 / Sequence 36, Application US/09844696
 / GENERAL INFORMATION:
 / APPLICANT: GEORGE, LISLE W.
 / APPLICANT: ANGELOS, JOHN A.
 / APPLICANT: HESS, JOHN F.
 / TITLE OF INVENTION: MORAXELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA
 / TITLE OF INVENTION: BOVIS INFECTIONS
 / FILE REFERENCE: 481_06
 / CURRENT APPLICATION NUMBER: US/09/684,696
 / CURRENT FILING DATE: 2001-06-19
 / NUMBER OF SEQ ID NOS: 41
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO: 36
 / LENGTH: 1428
 / TYPE: DNA
 / ORGANISM: Moraxella bovis
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (1) .. (1425)
 US-09-884-696-36

ALIGNMENTS

/ Sequence 1, Appli.
 / Sequence 121, Appli.
 / Sequence 270, Appli.
 / Sequence 1684, Appli.
 / Sequence 260, Appli.
 / Sequence 3629, Appli.
 / Sequence 1, Appli.
 / Sequence 3641, Appli.
 / Sequence 145, Appli.
 / Sequence 6676, Appli.
 / Sequence 97, Appli.
 / Sequence 120, Appli.
 / Sequence 87, Appli.
 / Sequence 4268, Appli.
 / Sequence 6611, Appli.
 / Sequence 2245, Appli.
 / Sequence 1336, Appli.
 / Sequence 135196, Appli.
 / Sequence 649, Appli.
 / Sequence 2093, Appli.
 / Sequence 9794, Appli.
 / Sequence 3389, Appli.
 / Sequence 105, Appli.
 / Sequence 12, Appli.
 / Sequence 12, Appli.
 / Sequence 12, Appli.
 / Sequence 12, Appli.
 / Sequence 4119, Appli.
 / Sequence 13, Appli.
 / Sequence 6015, Appli.
 / Sequence 10, Appli.
 / Sequence 11, Appli.
 / Sequence 12, Appli.
 / Sequence 12, Appli.
 / Sequence 12, Appli.
 / Sequence 12, Appli.

Sequence 109, App
 Sequence 79, Appli.
 Sequence 906, App
 Sequence 251, App
 Sequence 829, App
 Sequence 9, Appli.
 Sequence 39, Appli.
 Sequence 83, Appli.
 Sequence 6704, Appli.
 Sequence 1, Appli.
 Sequence 121, Appli.
 Sequence 270, Appli.
 Sequence 1684, Appli.
 Sequence 260, Appli.
 Sequence 3629, Appli.
 Sequence 1, Appli.
 Sequence 3641, Appli.
 Sequence 145, Appli.
 Sequence 6676, Appli.
 Sequence 97, Appli.
 Sequence 120, Appli.
 Sequence 87, Appli.
 Sequence 4268, Appli.
 Sequence 6611, Appli.
 Sequence 2245, Appli.
 Sequence 1336, Appli.
 Sequence 135196, Appli.
 Sequence 649, Appli.
 Sequence 2093, Appli.
 Sequence 9794, Appli.
 Sequence 3389, Appli.
 Sequence 105, Appli.
 Sequence 12, Appli.
 Sequence 12, Appli.
 Sequence 12, Appli.
 Sequence 12, Appli.
 Sequence 4119, Appli.
 Sequence 13, Appli.
 Sequence 6015, Appli.
 Sequence 10, Appli.
 Sequence 11, Appli.
 Sequence 12, Appli.
 Sequence 12, Appli.
 Sequence 12, Appli.
 Sequence 12, Appli.

Alignment Scores:

Pred. No.:	2.37e-23	Length:	1428
Score:	242.00	Matches:	50
Percent Similarity:	65.79%	Conservative:	25
Best Local Similarity:	43.86%	Mismatches:	39
Query Match:	39.80%	Indels:	0
DB:	11	Gaps:	0

US-09-484-577A-4 (1-124) × US-09-884-696-36 (1-1428)

Qy	10 SerAlaArgGluValValAlaValAlaGlyLysThrArgAspGluLeuAlaPheLeuPro	29	Length:	1428
Db	64 GCGTTGAGACCAACTAACCCCTCCATGGTACTAAAGAACTCCCTTCCTCTCT	123	Length:	1428
Qy	30 AlaAlaAlaGluLeuAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAlaLeu	49	Length:	1428
Db	124 GCACTCATCTGAGACTCAGACACCTGTATCCAGATCTTAAGTGACAGCTAGATA	163	Length:	1428
Qy	50 LeuAlaAlaLeuPhethyrrCysAlaValAlaAlaGlyLeuGlyArgLeuAspIleVal	69	Length:	1428
Db	184 ATATGATATTGTCCTATTCGTTGCTTGTTGCTGGTTGAGTTGACAGTTGATTTGTT	243	Length:	1428
Qy	70 AlaSerAlaSerArgLysIleValProGlyAspArgValLysLeuValGlnProLeuGlu	89	Length:	1428
Db	244 GCTACACCTTCAAGTAAATTCCTAGGCATGGCTAGCCATATTAAATCTTGGAA	303	Length:	1428
Qy	90 ValGlyAlaValAlaArgAlaThrHisValAlaGlyAspGlyGlyGlyLysIleAlaGlyLysIle	109	Length:	1428
Db	304 ACAGCGATAGTTAAAGCAAGTITATGTACGTCATGGTCAAATGTCAAACAGGTGAATA	363	Length:	1428
Qy	110 LeuIleGluLeuLeuAspPheAlaGlyGlyValAlaPheAla	123	Length:	1428
Db	364 CTAGTAGATTAGTGGAAATCGGTCAGATAGTGAGTGTGTC	405	Length:	1428

RESULT 2

US-10-085-959-109	Sequence 109, Application US/10085959
, Publication No. US20030165870A1	, GENERAL INFORMATION:
, APPLICANT: Blattner, Frederick R.	, APPLICANT: Welch, Rodney A.
, APPLICANT: Burland, Valerie D.	, TITLE OF INVENTION: No. US20030165870A1; Sequence of E. coli CFT073
, FILE REFERENCE: 960296_97649	CURRENT APPLICATION NUMBER: US/10/085,959
, CURRENT FILING DATE: 2002-03-01	PRIOR APPLICATION NUMBER: 60/242,412
, PRIOR FILING DATE: 2000-10-19	NUMBER OF SEQ ID NOS: 255
SOFTWARE: PatentIn version 3.1	SEQ ID NO: 109
LENGTH: 76804	TYPE: DNA
ORGANISM: Escherichia coli	FEATURE:
NAME/KEY: misc feature	LOCATION: (39751) . (39951)
OTHER INFORMATION: Unsure	NAME/KEY: misc feature
NAME/KEY: misc feature	LOCATION: (49372) . (49372)
OTHER INFORMATION: Unsure	NAME/KEY: misc feature
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LOCATION: (73751) . (73751)	OTHER INFORMATION: Unsure

OTHER INFORMATION: Unsure

NAME/KEY: misc feature

LOCATION: (73759) . (73759)

OTHER INFORMATION: Unsure

NAME/KEY: misc feature

LOCATION: (73761) . (73761)

OTHER INFORMATION: Unsure

NAME/KEY: misc feature

LOCATION: (73766) . (73766)

OTHER INFORMATION: Unsure

NAME/KEY: misc feature

LOCATION: (73774) . (73774)

OTHER INFORMATION: Unsure

NAME/KEY: misc feature

LOCATION: (73781) . (73781)

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NAME/KEY: misc feature

LOCATION: (73788) . (73788)

OTHER INFORMATION: Unsure

NAME/KEY: misc feature

LOCATION: (73802) . (73802)

OTHER INFORMATION: Unsure

US-10-085-959-109

Alignment Scores:

pred. No.:	6.11e-12	Length:	76804
Score:	176.00	Matches:	36
Percent Similarity:	60.78%	Conservative:	26
Best Local Similarity:	35.59%	Mismatches:	40
Query Match:	28.95%	Indels:	0
DB:	12	Gaps:	0

US-09-484-577A-4 (1-124) × US-10-085-959-109 (1-76804)

Qy

20 LysThrArgAspGluLeuIleValProAlaLeuPheLeuValGluIleValPheLeuProPro 39

Db

17983 CGTGAAGAAAGGAAATGAAATCTTACCGCTCATCGGAAATTATGAAAGCCGCTA 18042

Qy

40 SerProThrAlaArgLeuThrAlaAlaLeuPheThyCysAlaValAla 59

Db

18043 TCCAGACGGCCGCTCTGTTGCTTATTTATGGGTTCTGGTTATCTGCTTCATT 18102

Qy

60 TrpAlaGlyLeuGlyArgLeuAspIleValAlaSerAlaSerArgLysIleValProGly 79

Db

18103 TTATCTGTTAGTGGTCAGTGGTGAATGGAAATTACAATCACTAAGT 18162

Qy

80 AspArgValysIleValGlnIlePheLeuGluValGlyValArgAlaThrIleValArg 99

Db

18163 GGGCGAGCAAGAAATTAAACCTATTGAAACTAAATGTAAGAAATTTGTAAAA 18222

Qy

100 AspGlyGlnThrVallysAlaGlyGluIleLeuIleAspProPheAlaGlyGly 119

Db

18223 GAAGGAGAGTGAATCGGAAAGGGATCTGTATTAAAGCTTACAGGACTGGAGCTGAA 18282

Qy

120 ValAsp 121

Db

18283 GCTGAT 18288

RESULT 3

US-09-956-004-79/C

Sequence 79, Application US/09956004

Patent No. US2004072595A1

GENERAL INFORMATION:

APPLICANT: Patrick J. Dillon et al.

TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands

FILE REFERENCE: PB324D1

CURRENT APPLICATION NUMBER: US/09/956,004

PRIOR APPLICATION NUMBER: 60/061,953

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/061,953

PRIOR FILING DATE: 1997-10-14

PRIOR APPLICATION NUMBER: 60/031,626

PRIOR FILING DATE: 1996-11-22

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_P2n model

Run on: October 23, 2003, 11:14:20 ; Search time 57 Seconds

(without alignments)
960-202 Million cell updates/sec

Title: US-09-484-577a-4

Perfect score: 608

Sequence: 1 LSSLSPRMKSAREVYAVGGK..... KAGEILIEDPFAGGVDVAT 124

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
DelPop 6.0 , Delext 7.0

Searched: 569978 seqs, 220651566 residues

Total number of hits satisfying chosen parameters: 1139956

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line Parameters:

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6: /cgn2_6_ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Score	Query	Match	Length	DB	ID	Description
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c	2	215	35.4	28804	3	US-09-096-542-2		Sequence 2, Appli
c	3	215	35.4	28804	3	US-09-096-867-2		Sequence 3, Appli
c	4	169	27.8	5120	3	US-09-772-270A-6		Sequence 4, Appli
c	5	169	27.8	8370	4	US-09-062-126-1		Sequence 5, Appli
c	6	169	27.8	8370	4	US-08-772-270A-14		Sequence 6, Appli
c	7	168	27.6	7721	3	US-09-062-126-1		Sequence 7, Appli
c	8	154	25.3	3576	4	US-09-776-79-79		Sequence 8, Appli
c	9	117	19.2	1236	4	US-09-328-252-593		Sequence 9, Appli
c	10	109	17.9	1263	4	US-09-252-591A-13467		Sequence 10, Appli
c	11	109	17.9	1263	4	US-09-252-591A-13658		Sequence 11, Appli
c	12	104.5	17.2	1380	4	US-09-252-591A-3550		Sequence 12, Appli

Sequence 3557, Appli
Sequence 11544, Appli
Sequence 11665, Appli
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Sequence 39, Appli
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ALIGNMENTS

RESULT : US-09-592-874-1/c

Sequence 1, Application US/09592874
Parent No. 5854034

GENERAL INFORMATION:

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESS: JULES E. GOLDBERG
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA

ZIP: 10016-2391

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09592,874

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/377,440

FILING DATE: 24-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: GOLDBERG, JULES E.

REGISTRATION NUMBER: 24,408

TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6
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and is derived by analysis of the total score distribution.

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REFERENCE Zhan, F.H. and Li, G.Y.
AUTHORS Unpublished
TITLE Differentially expressed cDNA sequence
JOURNAL Contact: Zhan FH
Cancer Research Institute
88 Xiangya Road, Changsha, Hunan, 410078, China.
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AUTHORS Cloning of genes related to Chlorophyllin Antitransforming Against
Title Cloning of genes related to Chlorophyllin Antitransforming Against
JOURNAL Zhongl lu Fangzhi Zazhi 10 (1), 31-34 (2003)
COMMENT Contact: Lijin Z
Institute for Chemical Carcinogenesis
Guangzhou Medical College
195 Dongfengxi Road, Guangzhou 510182, China
Tel: 8620 81340186
Email: lijin_zhu@hotmail.com
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REFERENCE 1 (bases 1 to 178)
AUTHORS Warachit,J., Portantakasem,W. and Mutirangura,A.
TITLE Identification of differentially methylated sequence between white blood cells and sperm
JOURNAL Unpublished
COMMENT Contact: Warachit J.
Medical Oncology Unit, Faculty of Medicine
Chulalongkorn University
Prathumwan Rd., Bangkok, Thailand, 10330
Tel: 662-256-4532
Fax: 662-256-4534
Email: jiranun_w@hotmail.com
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GenCore version 5.1.6
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C 3	24	4.8	60	24	AAD32137	Sau3AI DNA fragment
C 4	24	4.8	60	24	AAD32137	Sau3AI DNA fragment
5	21	4.2	24	15	AA065644	Primer/adaptor use
6	21	4.2	24	17	AAT13201	Primer R_Bam 24 us
7	21	4.2	24	19	AAV03563	Probe RBam24 for S
8	21	4.2	24	20	AAZ24707	Adaptor sequence r

9	2:	4.2	24	20	AAZ21386	Primer R_Bam-24 fo
10	11	4.2	24	21	AAZ92275	Oligonucleotide #7
11	12	4.2	24	22	AB088731	Oligonucleotide SE
12	13	4.2	24	22	ABA98733	RDA primer R_Bam14
13	14	4.2	24	24	AA1729451	Primer R_Bam24, se
14	15	4.2	24	24	AA1729456	Sau3AI DNA fragmen
15	16	4.0	23	22	AAH23398	Nucleotide sequenc
16	17	4.0	24	18	AAV92397	Adapter primer RA2
17	18	4.0	24	18	AAV92398	Adapter primer RC22
18	19	4.0	24	18	AAV92401	Adapter primer RA2
19	20	4.0	24	18	AAV92403	Adapter primer RC22
20	21	4.0	24	19	AAV03566	Probe RMSP24 for S
21	22	4.0	24	19	AAV05432	Primer used in pro
22	23	4.0	24	19	AAV05434	Primer used in pro
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27	28	4.0	24	19	AAV05441	Primer RC24 used
28	29	4.0	24	19	AAV05441	Primer RA24-U used
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31	32	4.0	24	20	AAV24299	Human c1R BspHI-IC
32	33	4.0	24	21	AAV72895	Yeast PCR primer #
33	34	4.0	24	21	AAV72897	Yeast PCR primer #
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38	39	4.0	24	21	AAV73460	Yeast PCR primer R
39	40	4.0	24	21	AAV73462	Yeast PCR primer R
40	41	4.0	24	21	AAV73462	Sequencing and PCR
41	42	4.0	24	21	AAV55870	Tsp 509 I adapter
42	43	4.0	24	21	AAV55872	Hind III adapter p
43	44	4.0	24	21	AAV55874	Adapter primer nuc
44	45	4.0	24	21	AAV55894	Adapter primer nuc
45	46	4.0	24	21	AAV55908	Adapter primer nuc
46	47	4.0	24	21	AAV55948	Adapter primer nuc
47	48	4.0	24	21	AAV55950	Adapter nucleotide RX
48	49	4.0	24	21	AAV00452	Sample adapter pri
49	50	4.0	24	21	AAV28891	RTaqI adapter
50	51	4.0	24	21	AAV28892	Sau3A I enzyme amp
51	52	4.0	24	22	AAE27247	BsaW I enzyme amp
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53	54	4.0	24	24	AAD5473	Hind III restrict
54	55	4.0	24	24	AAD45475	Primer R_Bgl 24 us
55	56	4.0	24	24	AAD45477	Human Fanconi anae
56	57	4.0	24	24	AAD45497	Represenational d
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63	64	3.8	23	19	AAV27826	Non-biotinylated P
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75	76	3.8	24	21	AAV28819	R_Bgl 24 PCR prime
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77	78	3.8	24	21	AAV295366	Oligonucleotide
78	79	3.8	24	21	AAV288523	Murine Ha3 gene pr
79	80	3.8	24	21	AAV236285	Oligonucleotide pr
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GenCore version 5.1.6						
Copyright (C) 1993 - 2003 CompuGen Ltd.						
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ALIGNMENTS

RESULT 1

US-09-631-349A-19

; Sequence 19, Application US/09631349A

; Patent No. 6455255

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Birkenmeyer, Larry G.

; APPLICANT: Leary, Thomas P.

; APPLICANT: Muerhoff, A. Scott

; APPLICANT: Desai, Suresh M.

; APPLICANT: Mushahwar, Isa K.

; TITLE OF INVENTION: METHOD OF PERFORMING SUBTRACTIVE HYBRIDIZATION

; FILE REFERENCE: 6714.US.OI

; CURRENT APPLICATION NUMBER: US/09/631,349A

; CURRENT FILING DATE: 2000-08-02

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 19

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Primer R-Bam 24

; NAME/KEY: misc_feature

; LOCATION: (29)....(32)

; OTHER INFORMATION: n = a or g or c or t/u, unknown or other at other positions 29-32

US-09-631-349A-19

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Best Local Similarity 100.0%; Pred. No. 0 C06; Length 60;

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Db 4 ACTCTCCAGCCTCTCACCGAGAT 27

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US-09-631-349A-19.C

; Sequence 19, Application US/09631349A

; Patent No. 6455255

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Birkenmeyer, Larry G.

; APPLICANT: Leary, Thomas P.

; APPLICANT: Muerhoff, A. Scott

; APPLICANT: Desai, Suresh M.

; APPLICANT: Mushahwar, Isa K.

; TITLE OF INVENTION: METHOD OF PERFORMING SUBTRACTIVE HYBRIDIZATION

; FILE REFERENCE: 6714.US.OI

; CURRENT APPLICATION NUMBER: US/09/631,349A

; CURRENT FILING DATE: 2000-08-02

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 19

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Primer R-Bam 24

; NAME/KEY: misc_feature

; LOCATION: (29)....(32)

; OTHER INFORMATION: n = a or g or c or t/u, unknown or other at other positions 29-32

US-09-631-349A-19.N

Query Match Score 4.8%; Score 24; DB 4; Length 60;

Best Local Similarity 100.0%; Pred. No. 0 C06; Length 60;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTCTCCAGCCTCTCACCGAGAT 24

Db 4 ACTCTCCAGCCTCTCACCGAGAT 27

RESULT 3

US-09-631-349A-21

; Sequence 21, Application US/09631349A

; Patent No. 6455255

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Birkenmeyer, Larry G.

; APPLICANT: Leary, Thomas P.

; APPLICANT: Muerhoff, A. Scott

; APPLICANT: Desai, Suresh M.

; APPLICANT: Mushahwar, Isa K.

; TITLE OF INVENTION: METHOD OF PERFORMING SUBTRACTIVE HYBRIDIZATION

; FILE REFERENCE: 6714.US.OI

; CURRENT APPLICATION NUMBER: US/09/631,349A

; CURRENT FILING DATE: 2000-08-02

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 21

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Primer R-Bam 19N

US-09-631-349A-21/c

; Sequence 21, Application US/09631349A

; Patent No. 6455255

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Birkenmeyer, Larry G.

; APPLICANT: Leary, Thomas P.

; APPLICANT: Muerhoff, A. Scott

; APPLICANT: Desai, Suresh M.

; APPLICANT: Mushahwar, Isa K.

; TITLE OF INVENTION: METHOD OF PERFORMING SUBTRACTIVE HYBRIDIZATION

; FILE REFERENCE: 6714.US.OI

; CURRENT APPLICATION NUMBER: US/09/631,349A

; CURRENT FILING DATE: 2000-08-02

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSEQ for Windows Version 4.0

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; LENGTH: 60

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Primer R-Bam 19N

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C	47	7	5.6	116	193426 Sequence
C	48	7	5.6	116	195044 Sequence
C	49	7	5.6	116	195052 Sequence
C	50	7	5.6	116	195053 Sequence

51	7	5.6	125	6	AR140737 Sequence	REFERENCE	2 (bases 1 to 231)
52	7	5.6	125	6	I93416 Sequence 14	AUTHORS	Lee,R.H. and Chen,S.C.G.
53	7	5.6	125	6	I93416 Sequence 14	TITLE	Direct Submission
54	7	5.6	125	6	I95043 Sequence 14	JOURNAL	Submitted (01-MAR-2001) Institute of Botany, Academia Sinica, Taipei 11529, Taiwan
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56	7	5.6	129	6	AX526985 Sequence	source	1..231
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58	7	5.6	159	6	BD028280 Sequence	/mol type="mRNA"	
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66	7	5.6	197	14	AF2722009 HIV-1 iso	/product="unknown protein"	
67	7	5.6	203	14	X05821 Human T-lym	/protein_id="P0AL6-875.1"	
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100	6	4.8	249	14	191429 Sequence 62	Title	
			20	6	AY655508 Sequence	Sequence-specific detection of nucleic acid hybrids using a perfect	
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							58 ValAlaTrpAlaGlyLeuGly 64
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CM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 13:28:22 ; Search time 1724 Seconds
 (without alignments)
 1748.118 Million cell updates/sec

29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Ygapop 60.0 ; Ygapext 60.0	6	6.5	244	12	BM76055 if87b01.y
	Fgapop 6.0 ; Fgapext 7.0	7	5.6	239	28	AZ853380 M0156J03
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Model

nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 12:35:16 ; Search time 235 Seconds
(without alignments)
1424.384 Million cell updates/sec

Title: US-C9-484-577A-4

Perfect score: 124

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Word size: 1

Total number of hits satisfying chosen parameters: 3106038

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match	Length	DB ID	Description
	1	7	5.6	33	17	AAT30598 Target binding reg HIV-1 LTR region c
	2	7	5.6	36	14	AAQ3247 HIV-1 LTR - cores
	3	7	5.6	38	13	AAQ3271 HIV-1 LTR mutation
	4	7	5.6	43	12	AAQ12253 EcorI-AluNI linker
	5	7	5.6	43	12	AAQ85352 Target binding reg bx11 gene 5' end c
	6	7	5.6	45	17	AAT30611 HIV-1 LTR mutation
	7	7	5.6	47	24	AAD2073 Rennin gene probe.
	8	7	5.6	48	12	AAQ14775 Linker used to mak EcorI-AluNI linker
	9	7	5.6	49	22	AAC86358 Linker used to mak HIV wild type PILI
	10	7	5.6	50	22	AAC86351 Sau3A DNA fragmen
	11	7	5.6	56	22	AAC86357 Sau3A DNA fragmen
	12	7	5.6	59	17	AAT30612 Target binding reg Sau3A DNA fragmen
	13	7	5.6	59	17	AAT30612 Target binding reg Sau3A DNA fragmen
	14	7	5.6	60	21	AAT15068 Target binding reg Oligonucleotide us
	15	7	5.6	60	21	Oligo_BET-039 to 9
	16	7	5.6	60	24	AAD00174 Sau3A DNA fragmen
	17	7	5.6	60	24	AAD2135 Sau3A DNA fragmen
	18	7	5.6	60	24	AAD32135 Sau3A DNA fragmen
	19	7	5.6	60	24	AAD32137 Sau3A DNA fragmen
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	21	7	5.6	70	17	AAT30614 Transforming growth factor
	22	7	5.6	70	17	AAT30617 Probe nucleic acid
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	59	7	5.6	189	18	Human GDP-mannose
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	61	7	5.6	200	19	Human lung specific
	62	7	5.6	210	24	Human GDP-mannose
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	64	7	5.6	216	12	Strawberry fruit r
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Sequence 18, APP

130

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

RESULT 1
; Sequence 18, Application US/08860844
; GENERAL INFORMATION:
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 372-5800
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: Linear

RESULT 2
; Sequence 18, Application US/08860844
; GENERAL INFORMATION:
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/407,543
; FILING DATE: 03-Apr-2003
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US-10-0852-000-2
; FILING DATE: 09-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: Linear

RESULT 3
; Sequence 18, Application US/08860844
; GENERAL INFORMATION:
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: Linear

Result No.	Score	Query	Match	Length	DB	ID	Description	%
1	21	4.2	24	10	US-09-928-457-55		Sequence 55, Appl.	
2	21	4.2	24	14	US-10-193-51A-13		Sequence 13, Appl.	
3	21	4.2	28	9	US-09-751-561-55		Sequence 55, Appl.	
4	20	4.0	23	9	US-09-755-398A-2		Sequence 2, Appl.	
5	20	4.0	24	9	US-09-751-561-1		Sequence 1, Appl.	
6	20	4.0	24	9	US-09-751-561-15		Sequence 15, Appl.	
7	20	4.0	24	10	US-09-928-457-58		Sequence 58, Appl.	
8	20	4.0	24	11	US-09-389-164-1		Sequence 1, Appl.	
9	20	4.0	24	11	US-09-989-164-5		Sequence 5, Appl.	
10	20	4.0	24	11	US-09-989-364-19		Sequence 19, Appl.	
11	20	4.0	24	14	US-10-193-51A-25		Sequence 25, Appl.	
12	20	4.0	24	14	US-10-001-570-27		Sequence 27, Appl.	
13	20	4.0	24	14	US-10-001-570-29		Sequence 29, Appl.	
14	20	4.0	24	14	US-10-001-570-31		Sequence 31, Appl.	
15	20	4.0	24	14	US-10-001-570-33		Sequence 33, Appl.	
16	20	4.0	24	14	US-10-001-670-53		Sequence 53, Appl.	
17	20	4.0	20	19	US-10-001-670-67		Sequence 67, Appl.	
18	20	4.0	20	19	US-10-001-670-07		Sequence 107, Appl.	
19	20	4.0	20	19	US-09-751-561-109		Sequence 57, Appl.	
20	20	4.0	20	19	US-09-751-561-59		Sequence 59, Appl.	
21	20	4.0	22	19	US-10-191-438-2		Sequence 2, Appl.	
22	20	3.8	19	19	US-10-191-438-4		Sequence 4, Appl.	
23	20	3.8	19	19	US-08-424-550B-1		Sequence 1, Appl.	
24	20	3.8	19	19	US-09-751-297-1		Sequence 1, Appl.	
25	19	3.8	19	19	US-09-751-334-7		Sequence 7, Appl.	
26	19	3.8	19	19	US-10-096-534-69		Sequence 6, Appl.	
27	19	3.8	19	19	US-10-134-245-7		Sequence 7, Appl.	
28	19	3.8	19	19	US-10-348-190-22		Sequence 22, Appl.	
29	19	3.8	19	19	US-10-160-237-11		Sequence 11, Appl.	
30	19	3.8	19	19	US-10-032-626-7		Sequence 7, Appl.	
31	19	3.8	19	19	US-10-191-438-3		Sequence 6, Appl.	
32	19	3.8	19	19	US-10-067-13-6		Sequence 11, Appl.	
33	19	3.8	19	19	US-10-085-108-11		Sequence 4, Appl.	
34	19	3.8	19	19	US-10-235-264-4		Sequence 7, Appl.	
35	19	3.8	19	19	US-10-193-451A-7		Sequence 19, Appl.	
36	19	3.8	19	19	US-09-908-75-483		Sequence 5483, Appl.	
37	19	3.8	19	19	US-09-908-975-18740		Sequence 18740, Appl.	
38	19	3.8	19	19	US-09-908-975-18740		Sequence 3, Appl.	
c	39	19	3.8	19	US-09-791-244-3		Sequence 8, Appl.	
c	40	19	3.8	19	US-09-758-735-8		Sequence 12, Appl.	
c	41	17	3.4	20	9		Sequence 18749, Appl.	
c	42	17	3.4	20	9		Sequence 300, Appl.	
c	43	17	3.4	60	12		Sequence 1201, Appl.	
c	44	17	3.4	103	10		Sequence 486, Appl.	
c	45	17	3.4	103	10		Sequence 1007, Appl.	
c	46	17	3.4	103	10		Sequence 145, Appl.	
c	47	17	3.4	103	10		Sequence 57, Appl.	
c	48	17	3.4	103	12		Sequence 210, Appl.	
c	49	17	3.4	103	12		Sequence 568, Appl.	
c	50	16	3.2	17	12		Sequence 1272, Appl.	
c	51	16	3.2	17	12		Sequence 23, Appl.	
c	52	15	3.0	17	12		Sequence 106, Appl.	
c	53	15	3.0	17	12		Sequence 10, Appl.	
c	54	15	3.0	19	12		Sequence 3944, Appl.	
c	55	15	3.0	19	12		Sequence 96190, Appl.	
c	56	15	3.0	25	14		Sequence 29443, Appl.	
c	57	15	3.0	25	14		Sequence 27258, Appl.	
c	58	15	3.0	87	9		Sequence 257, Appl.	
c	59	15	3.0	179	9		Sequence 3378, Appl.	
c	60	15	3.0	237	10		Sequence 11230, Appl.	
c	61	15	3.0	237	10		Sequence 75923, Appl.	
c	62	15	3.0	25	14		Sequence 6, Appl.	
c	63	15	3.0	248	10		Sequence 3631, Appl.	
c	64	15	3.0	249	10		Sequence 106023, Appl.	
c	65	14	2.8	25	14		Sequence 6, Appl.	
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c	68	14	2.8	29	12		Sequence 8, Appl.	
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c	72	14	2.8	34	11		Sequence 8, Appl.	
c	73	14	2.8	34	11		Sequence 8, Appl.	
c	74	14	2.8	38	12		Sequence 141, Appl.	
c	75	14	2.8	38	12		Sequence 142, Appl.	
c	76	14	2.8	38	12		Sequence 147, Appl.	
c	77	14	2.8	38	12		Sequence 148, Appl.	
c	78	14	2.8	40	12		Sequence 47, Appl.	
c	79	14	2.8	60	10		Sequence 8, Appl.	
c	80	14	2.8	60	10		Sequence 2088, Appl.	
c	81	14	2.8	85	9		Sequence 5003, Appl.	
c	82	14	2.8	88	10		Sequence 500, Appl.	
c	83	14	2.8	88	14		Sequence 1860, Appl.	
c	84	14	2.8	105	10		Sequence 22266, Appl.	
c	85	14	2.8	119	9		Sequence 21451, Appl.	
c	86	14	2.8	117	9		Sequence 21357, Appl.	
c	87	14	2.8	139	9		Sequence 1171, Appl.	
c	88	14	2.8	143	9		Sequence 23978, Appl.	

Post-processing: Listing first 100 summaries
Published Applications NA:
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2: /cgn2_6/prodata/1/pubpna/PCT_FEW_PUB.seq:**
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4: /cgn2_6/prodata/1/pubpna/US006_PUBCOMB.seq:**
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Post. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Total number of hits satisfying chosen parameters: 1468544

Minimum DB seq length: 0

Maximum DB seq length: 250

Post-processing: Listing first 100 summaries

Published Applications NA:
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16: /cgn2_6/prodata/1/pubpna/US60C_PUBCOMB.seq:**

Score: Greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score: Greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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 C 91 14 2.8 157 10 US-09-878-574-8329
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 Sequence 8329, Ap1
 Sequence 9404, Ap1
 Sequence 19181, A
 Sequence 21030, A
 Sequence 9546, Ap1
 Sequence 7865, Ap1
 Sequence 8040, Ap1
 Sequence 7865, Ap1
 Sequence 8040, Ap1
 Sequence 1469, Ap1

ALIGNMENTS

RESULT 1

US-09-928-457-55

; Sequence 55, Application US/09928457

; Patent No. US2002016463A1

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION:

; TITLE OF INVENTION:

; TITLE OF INVENTION:

; NUMBER OF SEQUENCES: 99

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (OEB)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/928,457

; FILING DATE: 2001-08-14

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/214,759

; FILING DATE: 1991-12-10

; INFORMATION FOR SEQ ID NO: 55:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 base pairs

; TYPE: nucleotide

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; US-09-928-457-55

Query Match 4.2%; Score 21; DB 1C; Length 24;

Best Local Similarity 100.0%; Pred. No. 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

RESULT 2

US-10-193-451A-13

; Sequence 13, Application US/10193451A

; GENERAL INFORMATION:

; APPLICANT: KUNERT, KARL

; APPLICANT: RADEMAN, CHRISTOPHER A.

; APPLICANT: RADEMAN, SAMANTHA

; TITLE OF INVENTION: METHOD FOR FINDING GENETIC MARKERS

; FILE REFERENCE: 02831560005

; CURRENT FILING DATE: 2002-07-11

; PRIOR APPLICATION NUMBER: US/09/292,646

; PRIOR FILING DATE: 1993-04-15

; NUMBER OF SEQ ID NOS: 32

C 90 14 2.8 156 9 US-09-736-969A-65
 C 91 14 2.8 157 10 US-09-878-574-8329
 Sequence 65, App1
 Sequence 8329, Ap1
 Sequence 9404, Ap1
 Sequence 19181, A
 Sequence 21030, A
 Sequence 9546, Ap1
 Sequence 7865, Ap1
 Sequence 8040, Ap1
 Sequence 7865, Ap1
 Sequence 8040, Ap1
 Sequence 1469, Ap1

; OTHER INFORMATION:

; PUBLIC INFORMATION:

US-10-193-451A-13

; OTHER INFORMATION:

; PUBLIC INFORMATION:

US-09-928-457-55

; Sequence 55, Application US/09928457

; Patent No. US2002016463A1

; GENERAL INFORMATION:

; APPLICANT: Rothberg, Jonathan

; APPLICANT: Deem, Michael

; APPLICANT: Simpson, John

; TITLE OF INVENTION: Method for the Determination and

; TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without

; TITLE OF INVENTION: Sequencing

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESS: Pennie and Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOSS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/751,562

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/751,562

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Mistock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 79334-015-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)-790-9090

; TELEX: (212)-869-8864

; INFORMATION FOR SEQ ID NO: 55:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; US-09-928-457-55

; Query Match 4.2%; Score 21; DB 9; Length 28;

; Best Local Similarity 100.0%; Pred. No. 0; Gaps 0;

; Matches 21; Conservative 0; Mismatches 0; Indels 0;

; Gaps 0;

